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Afu 1 -----MMADKSKLVTPLKKTLENDLNDRLSLSAQKTERLLRLREYGTNPSNAGLI
Ani 1 -----MDLRILQCESEKIQVAKLINSLEKDIKDNLSLSAQRTQI LLQLRQYGTSPDNAGSI
Pch 1 -----MAPLQMGCEPAKIQVAVLQKLSLEEDQENNLSLADRIQT LLQLRQHGTMETNAEPI
Ptr 1 -----MSQKCEPAKIQVAVLQKLSLEKADLQAKQLSEORRKLLEQLKVVGRLVDMSDPI
Ncr 1 -----MASIQWCEPAKIQVAVLQKLSLEKADLQAKQLSEORRKLLEQLKVVGRLVDMSDPI
Gze 1 MATLPPAGLFGTDRKLEYKRLINDLSSEDI NEELYLPDDRAAVLDQLKILTRDPIINADPL

Afu 51 VSEWGMKILCRYGVEGETEDVRRRAALRCVANALLLDKMRQIFADTGYGSKLAEMLKCDN
Ani 57 VSKKGIELSKRYGIDGETTDVREAAALRCVANALLLDNMRQLFVDTGKGGRLAEMLKCDSD
Pch 57 YSQNGINTLMRYGVEGETEDVRRRAALRCVANALLLDPKMROAFVDTGYSGKLAEKLKTED
Ptr 55 FTEDGERTLGRCAFDEGETTPASQELRCVANALLLPKTRQIFVLDLGHGPHAAEKLKSDS
Ncr 55 FTKQGIETLTKHAFDGPSETTSPALAVLGNAMLLIPETRQRQFVLDLGYESKACEKLNNDN
Gze 61 YTEKGIETLTKHAYDKPSTKKSADAAARVLANAMVLLKTVTTRDIFVYKKGFAFNACQGLNGGS

Afu 111 SEDEMVISRILFLCTYDTHDYZEQLIKNHSLGDNVNYQIIRHAKQFPKSGRKP----LVQ
Ani 117 SEHEMVISRILFLSTYDTHNFDLIDLINNHSLGDNVNYQILRHASKQFPKSGRKP----LSQ
Pch 117 SEDEMVISRILFYATYNTLDEKDLIKSHALGDNVNYQILRHAKQFPKSGRKP----LSQ
Ptr 115 IDEFLAARVLFYNTYDANLDYAOIQRONQLADSIINAARHAKQFPKSGRKPSPQHTQP
Ncr 117 WDEFLAARVLFYNTYDANLDYAOIQRONQLADSIINAARHAKQFPKSGRKPSPQHTQP
Gze 121 FEDEFINSRILFLSTYGRVLDLKKLIDDERGLADRISENLARHAK-----ESKAK----SDP

Afu 167 IDEHALFTDLKLVFNVSKVYVVDLSATFSPSIPYIFKIIISRIDIP----PKPLDGLLGYLL
Ani 173 VDEHALFTDLKLVFNVSKVYVVDLSATFSPSIPYIFKIIISRIDIP----LKPLDGLLGLTLL
Pch 173 MDEHALSDTLKLVFNVSKVYVVDLSATFSPSIPYIFKIIISRIDIP----AKPLDGLVGGLL
Ptr 175 HELMALSETLKLNVNVIHFHKLQSLPFTSIPNVFRMLVSRNPS----SPPLATPTRELV
Ncr 175 HELMALGETLKLNVNVIHFKQSKLDCFTAAVPHIVTLLSLDIPPPKGTBPPLSPPLSLV
Gze 173 HQDMALVESAKILFRVITYCPKESSTSAIPHVLVALLLKQDIS----QTKPLDPPVGFII

Afu 223 NCLSTLDLENKGFHFESPIFPFNFQNCNVDKLINILDOAVSAYDAQDLATKAIPLLHT
Ani 229 NCLSTLDLENKGFHFESPIFPFNFQNCNVDKLINILDOAVSAYEFSLETKAIPLFHT
Pch 229 NTLSTLDLENKGFHFESPIFPFNFQNCNVDKLVSILOQATSIYSPTELEANAVPLLYS
Ptr 231 NALLHLDLEDPGQ----KAVFPPFDNVNITCLVTLTLLKAIIVYPPKELDDTITPVITL
Ncr 235 NALMNLRLDSEEAR----CLYPKDAPSSSLAEKLTLLDLSLKAYSDDQELDATVTPIVCI
Gze 230 NALANLLVGSSDCQ----KSHPEEEDPEKVVSRSLISILDAAMKNVDPNQLDATVSPLLGV

Afu 283 LVTIYEVAPDGP--RKYMQWLLLPEDSDRKPPIGKSDTLSSKLLRLSTTFYQN-LKIAIS
Ani 289 LVTIYEVAPDGP--RKYMQWLLLPEDDNRDRPIGQSDTLSSKLLRLSTMHYAN-LKVAIS
Pch 289 LIAYIEVAPDGP--RKYMQWLLLPEDDTRSLPIGQSDTLSSKLLRLSTTHFAN-LKVTIS
Ptr 287 LRRYIEVAPDGP--KQTKQTLLEPDAERDKPIGKSDTLSSKLLRLSTALTPTLRGSAIA
Ncr 291 ISSIYENASDPPVDEIRKSLPSEERNKVILGKGDTLPAKLLANMNTPIAPEFARVAIS
Gze 286 ISSVYKHAPESS--RKYIREKLLPTEEDRKEVILGKGDALSAKLLQNFNNELAPSVGTVIQ

Afu 340 EIMNFVLSGKDAE NLTKNIGYGFAAGL LASRGLPIPIQSAS-----EAFATNSNSFDPEINP
Ani 346 EIMNFVLSGKDAE NLTKNIGYGFAAGL LASRGMIPKSA-----EAFATNSQDLNPEINP
Pch 346 EIMNFVLSGKDAE NLTKNIGYGFAAGL LAARGTEMPQSA-----EASSAK-DGPDARNP
Ptr 345 SMLLELSQKIPATFVFNIGYGFAAGL ILSNNIEMPDDEVV-----KANAGKIDEAIPVNP
Ncr 351 HLLNWSLKDANKFVFNIGYGFAAGL IFQNNIIPVBEGLGGDAEKGSQAGQSSRRVNP
Gze 344 HLLYLDLSENDANKFVFNIGYGFAAGL IFQNNIIPVBEGLGGDAEKGSQAGQSSRRVNP

Afu 395 ITGORWDAEKQDTGPPMRSEKEREAEERL FVLFERAKANGCLGNVENPVROAVESGRFEEL
Ani 401 ITGORWDAEKQDTGPPMRSEKEREAEERL FVLFERAKANGCLGNVENPVTOALREGRFEEL
Pch 400 ITGORWDAEKQDTGPPMRSEKEREAEERL FVLFERAKANGCLGNVENPVTOALREGRFEEL
Ptr 400 ITGORWDAEKQDTGPPMRSEKEREAEERL FVLFERAKANGCLGNVENPVTOALREGRFEEL
Ncr 411 ITGCFLDRETFVQTEPMQSEKEREAEERL FVLFERAKANGCLGNVENPVAKAVCEGRFEEL
Gze 393 VTGCHVDAEKQDTGPPMRSEKEREAEERL FVLFERAKANGCLGNVENPVTOALREGRFEEL

Afu 455 PDSDESD--
Ani 461 PDSDESD--
Pch 460 PDDDESD--
Ptr 460 DDDDESD--
Ncr 471 PDDVEEDSD
Gze 453 RDDVEEIE

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FIG S1 Alignment of RicA-like proteins in *A. fumigatus* (Afu), *A. nidulans* (Ani), *Penicillium chrysogenum* (Pch), *Pyrenophora tritici* (Ptr), *Neurospora crassa* (Ncr) and *Gibberella zeae* (Gze). ClustalW (<http://align.genome.jp/>) and BoxShade 3.21 (http://www.ch.embnet.org/software/BOX_form.html) were used for the alignment and presentation.

Table S1. Oligonucleotides used in this study

Name	SEQUENCE (5'→3')	Purpose
oNK-393	ATATGAATTCATGGATTTGCGTATTCTGCAGGGC	5' <i>Anr</i> A with <i>Eco</i> RI
oNK-394	ATATGCGGCCGCTTCACTATCAGAGTCAGGCAACTC	3' <i>Anr</i> A with <i>Not</i> I
oNK-521	ATATGGATCCTTATTCACTATCAGAGTCAGGCAAC	3' <i>Anr</i> A with <i>Bam</i> HI
oNK-507	ATATGGATCCTAATGGGTTGTGGAATGAGTACCGAG	5' <i>Anf</i> adA with <i>Bam</i> HI
oNK-508	ATATCTCGAGTTAAATCAGACCACAGAGTCTCAG	3' <i>Anf</i> adA with <i>Xho</i> I
oNK-509	ATATGGATCCTAATGGGTTGTATGAGCTCAAAGCAG	5' <i>Ang</i> anA with <i>Bam</i> HI
oNK-510	ATATCTCGAGTTAGAGTATGAGCGTGTGGAGATTC	3' <i>Ang</i> anA with <i>Xho</i> I
oNK-511	ATATGAATTCATGGGGTCGTGTTTCAGTTCAGAA	5' <i>Ang</i> anB with <i>Eco</i> RI
oNK-512	ATATGTCGACTTACAGGATCCCCGAGTCTTTCAA	5' <i>Ang</i> anB with <i>Sal</i> I
oNK-352	TAGTGCTTGGATGACAAGGTTTGT	5' flanking region of <i>Anr</i> icA
oNK-353	GCTTTGGCCTGTATCATGACTTCA AGAATACGCAAATCCATATTCACTC	3' <i>Anr</i> icA with <i>Afpyr</i> G tail
oNK-354	ATCGACCGAACCTAGGTAGGGTA AGAGCATCTATGGCAGAACATGAG	5' <i>Anr</i> icA with <i>Afpyr</i> G tail
oNK-355	ACCTACATACTGCGTATGTCTGCTG	3' flanking region of <i>Anr</i> icA
oNK-474	ACTTCTGCAGTCGGAATTGGCCTG AGAATACGCAAATCCATATTCACTC	3' <i>Anr</i> icA with <i>Anpyr</i> oA tail
oNK-475	TGGTGAGAACACATGCACAACCTG AGAGCATCTATGGCAGAACATGAG	5' <i>Anr</i> icA with <i>Anpyr</i> oA tail
oNK-356	TGGATGAACTCTGCAATCAGGCTC	5' nested of <i>Anr</i> icA
oNK-357	ATGCTTGCGTAAACCAAGCAAGTC	3' nested of <i>Anr</i> icA
oNK-397	AACGCAACGCAAAGGATAGCGAGC	5' flanking region of <i>Ansf</i> gA
oNK-398	ACTTCTGCAGTCGGAATTGGCCTG AGAGAAAGATCGACGGTGGGAGAG	3' <i>Ansf</i> gA with <i>Anpyr</i> oA tail
oNK-399	TGGTGAGAACACATGCACAACCTG TTGACCGGACCATACACCTCGCAC	5' <i>Ansf</i> gA with <i>Anpyr</i> oA tail
oNK-400	AGCAGACGTTCACTCAGAGCCACC	3' flanking region of <i>Ansf</i> gA
oNK-401	AATTTGGTAGTTGCGCCTACGGC	5' nested of <i>Ansf</i> gA
oNK-402	GTCGCAGAGGCGTAGCTCTACAG	3' nested of <i>Ansf</i> gA
oNK-412	TCACATCTCGATGATTGGTTGAATG	5' flanking region of <i>Anfl</i> bA
oNK-413	ACTTCTGCAGTCGGAATTGGCCTG TGGCATTGAAGAGTGCAGGTCGGAG	3' <i>Anfl</i> bA with <i>Anpyr</i> oA tail
oNK-414	TGGTGAGAACACATGCACAACCTG ACAGTAATTATCTACACGCGTGATG	5' <i>Anfl</i> bA with <i>Anpyr</i> oA tail
oNK-415	ACTACTCACTACCTAACTTGACTG	3' flanking region of <i>Anfl</i> bA
oNK-416	TGGTTGAATGGTGTATGGGTCAGC	5' nested of <i>Anfl</i> bA
oNK-417	TGTAGCTTTCGTTTCAGGCGATAGTG	3' nested of <i>Anfl</i> bA
oNK-870	ATATGGATCCTGCTTGGATGACAAGGTTTGTATCC	5' ge- <i>Anr</i> icA with <i>Bam</i> HI
oNK-871	ATATGCGGCCGCACCTACATACTGCGTATGTCTGCTG	3' ge- <i>Anr</i> icA with <i>Not</i> I
oJH-83	GGATGTATCGTGACTGGCCTTCGG	5' <i>Afpyr</i> G marker
oJH-86	TAATTCGCGGCATACGGTGTCTAA	3' <i>Afpyr</i> G marker

oNK-395	ATTCATGGGTGCTGTGCGAAAGG	5' <i>AnpyroA</i> marker
oNK-396	TTGCATCGCATAGCATTGCATTGC	3' <i>AnpyroA</i> marker
oNK-432	AGCGTCGGCTCGTCGCTCTCTCA	5' flanking region of <i>AnganB</i>
oNK-433	CTGCGCAGGCCGCCAACATCAAACATGCTGT	3' <i>AnganB</i> ^{Q208L}
oNK-434	GCGGCCTGCGCAGCGAGAGGAAAAAGTGGATTC	5' <i>AnganB</i> ^{Q208L}
oNK-435	TGACCACTCCGGCACTGGCATATG	3' flanking region of <i>AnganB</i>
oNK-436	ATATCCCGGGTCTTGCTCCGCAATCTGTATCCTG	5' nested of <i>AnganB</i> with <i>SmaI</i>
oNK-437	ATATGCGGCCGCTCGAATACCTGCCGGAACCTGC	3' nested of <i>AnganB</i> with <i>NotI</i>
oNK-540	TGTTCTGGATGATAGTCTTCTAG	5' flanking region of <i>AnrgsA</i>
oNK-541	ACTTCTGCAGTCGGAATTGGCCTG TTGACTGAACGTATCTTAAGAGTG	3' <i>AnrgsA</i> with <i>AnpyroA</i> tail
oNK-542	TGGTGAGAACACATGCACAACCTTG ACGTCGTGGCACAATCTTCCGGTG	5' <i>AnrgsA</i> with <i>AnpyroA</i> tail
oNK-543	AGCTCCAATACACTGCATGTGGAG	3' flanking region of <i>AnrgsA</i>
oNK-544	TGTCGCCGACCACTACTACTACC	5' nested of <i>AnrgsA</i>
oNK-545	TTGAACTATCTTAACGAGGGTGAC	3' nested of <i>AnrgsA</i>
oNK-562	TCATGTGCATTATGGAGCGTATTAG	5' flanking region of <i>AnrgsB</i>
oNK-563	ACTTCTGCAGTCGGAATTGGCCTG TGCTCTAGCAAGCTCGTGATGTTG	3' <i>AnrgsB</i> with <i>AnpyroA</i> tail
oNK-564	TGGTGAGAACACATGCACAACCTTG TGCCTTGAATCAGCATACAATCCAC	5' <i>AnrgsB</i> with <i>AnpyroA</i> tail
oNK-567	ACCTAGCTCTCTTCCAACGATGATC	3' flanking region of <i>AnrgsB</i>
oNK-605	TCTATTCAAGTTCTCAAACCTGCATC	5' nested of <i>AnrgsB</i>
oNK-606	AGCCCGCTGTGGCTCCGTAATCTC	3' nested of <i>AnrgsB</i>
oNK-568	ACATGCTTGACAAGACGAGAACTG	5' flanking region of <i>AnrgsC</i>
oNK-569	ACTTCTGCAGTCGGAATTGGCCTG TCCTCACCAAATCATATGCACAGC	3' <i>AnrgsC</i> with <i>AnpyroA</i> tail
oNK-603	TGGTGAGAACACATGCACAACCTTG ACTGTGAGTATGCTGCTTTTTATG	5' <i>AnrgsC</i> with <i>AnpyroA</i> tail
oNK-604	TACCTCGCTGGCTTCGAGTGGGAC	3' flanking region of <i>AnrgsC</i>
oNK-607	TCAAGAGCCTGCTGGTAGATATGG	5' nested of <i>AnrgsC</i>
oNK-608	AGAGTGCTGGACACGTCTCATTGT	3' nested of <i>AnrgsC</i>
oNK-14	ATATGAATTCATGAGTGCGGCGAACTATCCAG	5' <i>AnvosA</i> probe
oNK-15	ATATGTCGACTCACCGAGGAGTCCGTTTCGCTG	3' <i>AnvosA</i> probe
oNK-554	ATATAAGCTTATGGCCACTCTCTTTCACTCCGTC	5' <i>AnfluG</i> with <i>HindIII</i>
oNK-555	ATATGCGGCCGCATACCTCTCCACAAGCCACTTCCTG	3' <i>AnfluG</i> with <i>NotI</i>
oNK-556	ATATAAGCTTATGCGAAATCAGTCCAGCCTGTCC	5' <i>Anb1A</i> with <i>HindIII</i>
oNK-557	ATATGCGGCCGCTTCATCCCAGCCGTCAGGCTCAT	3' <i>Anb1A</i> with <i>NotI</i>
oNK-875	ATATCATATGCCTACTCTAGGAGTCTTTTGAAG	5' <i>AnpkaA</i> with <i>NdeI</i>
oNK-561	ATATGCGGCCGCGAAATCGGGGAACAGGTGACCGTG	3' <i>AnpkaA</i> with <i>NotI</i>
oNK-391	ATATGAATTCATGAAAATACTGGGTAGATACGGAG	5' <i>AfricA</i> with <i>EcoRI</i>
oNK-392	ATATGCGGCCGCCCTCTCAAAAAGCACGAATAACCTC	3' <i>AfricA</i> with <i>NotI</i>

oNK-358	TGGCGATATGGTCAAGCTACAAGG	5' flanking region of <i>Africa</i>
oNK-359	TTTGTAGGCTTTGGGCTGTTCAAA TGTGAGAGTCAGGACATACGCATC	3' <i>Africa</i> with <i>AnpyrG</i> tail
oNK-360	CTGATCTACCCCTTGGAACGCAGCA TGAGAGGTAAGACAAAGTTCCTAC	5' <i>Africa</i> with <i>AnpyrG</i> tail
oNK-361	ACACCAGGACTGACTCTGAGTATG	3' flanking region of <i>Africa</i>
oNK-933	AGTCAAATGAGGCCTCTAAACTGGTCA ATCATCGAGGCATACCTGCCATC	3' <i>Africa</i> with <i>AnargB</i> tail
oNK-934	AGCCAAGGTAGATCCAGGCCTAACACA ACAACACCTTGGAGCTATCAGTC	5' <i>Africa</i> with <i>AnargB</i> tail
oNK-362	CAGGCCAAGCTGAACATGCGAATG	5' nested of <i>Africa</i>
oNK-363	AGTTGTAGTCGCTAATCTTCTTCTC	3' nested of <i>Africa</i>
oBS-08	GCAATGTAAAGCTAACGTGCGTG	5' <i>AnpyrG</i> marker
oBS-09	TGCCTTTAAGCTTCGGGTAGAG	3' <i>AnpyrG</i> marker
oNK-104	ACACTTCAAAGGAGCGACGCTGTTG	5' <i>AnargB</i> marker
oNK-105	TCGACCTACAGCCATTGCGAAACCTC	3' <i>AnargB</i> marker
oNK-868	ATATGGATCCTGGCGATATGGTCAAGCTACAAGG	5' ge- <i>Africa</i> with <i>Bam</i> HI
oNK-869	ATATGCGGCCGCGCACACCAGGACTGACTCTGAGTATG	3' ge- <i>Africa</i> with <i>Nor</i> I
oNK-594	TGAGATCCCAGGGTAATATGTCTG	5' <i>AfbrlA</i> probe
oNK-595	TACTCATCCCATTCCATACTGATC	3' <i>AfbrlA</i> probe
oHS-382	AATTGTCGACTCATGGCTACTGACTGGCAGCCC	5' <i>AfabaA</i> probe
oHS-383	AATT GCGGCCGC TCATTGGACCGCCTCAGTTGC	3' <i>AfabaA</i> probe
oTL-7	ATATGGTACCATGTTTCGCTCAACCATTTCGATC	5' <i>AfwetA</i> probe
oTL-8	ATATGCGGCCGCGCAGAGGACAGCCTCCAGTGCTTC	3' <i>AfwetA</i> probe
